

Db 361 EKLOERLAKISGVAVIKVATGATETELKEKRIEDALNMTFAVVEEIVAGGITALNV 420
Oy 421 IEKVALELGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKIKNSPAGTFNAATG 480
Db 421 IEKVALELGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKIKNSPAGTFNAATG 480
Oy 481 EVMNDIKTGIIDPVKTSALONAAVASILITTEAVYANKPEPPATPPAPAPAGNDPM 540
Db 481 EVMNDIKTGIIDPVKTSALONAAVASILITTEAVYANKPEPPATPPAPAPAGNDPM 540
Oy 541 GGM 543
Db 537 GGM 539

RESULT 2
H98086
Chaperonin GroEL [Imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: H98086
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgelt, S.; Dehoff, B.S.; E
y, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McHenry, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H98086
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-540 <CUR>
A:Cross-references: GB:AE007317; PIDN:AA00525.1; PID:915459401; GSPDB:GN00174
C:Genetics:
A:Gene: groEL
C:Superfamily: chaperonin groEL

Query Match 88.1%; Score 2347; DB 2; Length 540;
Best Local Similarity 87.8%; Pred. No. 9.7e-110;
Matches 477; Conservative 34; Mismatches 28; Indels 4; Gaps 1;

Oy 1 MAKEIKFSADARAAYRGVMDLADTVKVTILGPKGRNVLEKAFGSPILITNDGVTIAKEIE 60
Db 1 MSKEIKFSADARAAYRGVMDLADTVKVTILGPKGRNVLEKAFGSPILITNDGVTIAKEIE 60
Oy 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPIGIRGIE 120
Db 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPIGIRGIE 120
Oy 121 TATATVAELKAIAPVSGKEAIAOVAASRSRSEKVEYISSEAMERKNGCVITTEESRG 180
Db 121 TATATVAELKAIAPVSGKEAIAOVAASRSRSEKVEYISSEAMERKNGCVITTEESRG 180
Oy 181 METELEVEEGNOFDRGYLSQYMTDNEMKADLENPILITDKKVSINIOELPLEEVK 240
Db 181 METELEVEEGNOFDRGYLSQYMTDNEMKADLENPILITDKKVSINIOELPLEEVK 240
Oy 241 TNRPLLIADVDGELPLVLNKIRGTENVVAVKAPGFGDRRKAMLEDAIILTGTVIT 300
Db 241 TNRPLLIADVDGELPLVLNKIRGTENVVAVKAPGFGDRRKAMLEDAIILTGTVIT 300
Oy 301 EDGLKELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSPDR 360
Db 301 EDGLKELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSPDR 360
Oy 361 EKLOERLAKISGVAVIKVATGATETELKEKRIEDALNMTFAVVEEIVAGGITALNV 420
Db 361 EKLOERLAKISGVAVIKVATGATETELKEKRIEDALNMTFAVVEEIVAGGITALNV 420
Oy 421 IEKVALELGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKIKNSPAGTFNAATG 480
Db 421 IEKVALELGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKIKNSPAGTFNAATG 480
Oy 541 GGM 543
Db 537 GGM 539

RESULT 3
B8674
60 kD chaperonin [Imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: B8674
R:Boletín, A.; Winkler, P.; Manger, S.; Jallón, O.; Malarme, K.; Welschenbach, J.; El
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: B8674
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-542 <STO>
A:Cross-references: GB:AE005176; PID:912723267; PIDN:AA04492.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: groEL
C:Superfamily: chaperonin groEL

Query Match 82.4%; Score 2195.5; DB 2; Length 542;
Best Local Similarity 81.1%; Pred. No. 3.4e-102;
Matches 442; Conservative 52; Mismatches 46; Indels 5; Gaps 3;

Oy 1 MAKEIKFSADARAAYRGVMDLADTVKVTILGPKGRNVLEKAFGSPILITNDGVTIAKEIE 60
Db 1 MSKEIKFSADARAAYRGVMDLADTVKVTILGPKGRNVLEKAFGSPILITNDGVTIAKEIE 60
Oy 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPIGIRGIE 120
Db 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPIGIRGIE 120
Oy 121 TATATVAELKAIAPVSGKEAIAOVAASRSRSEKVEYISSEAMERKNGCVITTEESRG 180
Db 121 TATATVAELKAIAPVSGKEAIAOVAASRSRSEKVEYISSEAMERKNGCVITTEESRG 180
Oy 181 METELEVEEGNOFDRGYLSQYMTDNEMKADLENPILITDKKVSINIOELPLEEVK 240
Db 181 METELEVEEGNOFDRGYLSQYMTDNEMKADLENPILITDKKVSINIOELPLEEVK 240
Oy 241 TNRPLLIADVDGELPLVLNKIRGTENVVAVKAPGFGDRRKAMLEDAIILTGTVIT 300
Db 241 TNRPLLIADVDGELPLVLNKIRGTENVVAVKAPGFGDRRKAMLEDAIILTGTVIT 300
Oy 301 EDGLKELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSPDR 360
Db 301 EDGLKELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSPDR 360
Oy 361 EKLOERLAKISGVAVIKVATGATETELKEKRIEDALNMTFAVVEEIVAGGITALNV 420
Db 361 EKLOERLAKISGVAVIKVATGATETELKEKRIEDALNMTFAVVEEIVAGGITALNV 420
Oy 421 IEKVALELGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKIKNSPAGTFNAATG 480
Db 421 IEKVALELGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKIKNSPAGTFNAATG 480
Oy 481 EVMNDIKTGIIDPVKTSALONAAVASILITTEAVYANKPEPPATPPAPAPAGNDPM 540
Db 481 EVMNDIKTGIIDPVKTSALONAAVASILITTEAVYANKPEPPATPPAPAPAGNDPM 540
Oy 541 GGM 543
Db 537 GGM 539

RESULT 4

JN0661

heat shock protein groEL - Lactococcus lactis subsp. lactis

C:Species: Lactococcus lactis subsp. lactis

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C:Accession: JN0661

R:Klm S.G., Batt, C.A.

Gene 127, 121-126, 1993

A:Title: Cloning and sequencing of Lactococcus lactis subsp. lactis groEL operon.

A:Reference number: JN0660; M0ID:93252268; PMID:8486277

A:Accession: JN0661

A:Molecule type: DNA

A:Residues: 1-542 <KIM>

C:Genetics:

A:Gene: groEL

C:Superfamily: chaperonin groEL

C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match

Best Local Similarity 81.5%; Score 2171.5; DB 2; Length 542;

Matches 438; Conservative 53; Mismatches 49; Indels 5; Gaps 3;

QY 1 MAKEKFSADARAAMRGVDMADPTVKTGLPGKRNVLKAFSGPLITNDGVTAKKE 60
 DB 1 MSKDIKFSDDARTAMRGIDILADVTITGLPGKRNVLKAFSGPLITNDGVTAKKE 60
 QY 61 LEHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120
 DB 61 LEHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120
 QY 121 TATATAVEALKAIAPVSGKEALIAOVAVSSRSSEKVEYISEAMERVNDGVITIEESRG 180
 DB 121 LAETVAVASIKEMAIPIVHDKSAIAQAVTSSRSSEKVEYISDAMERVNDGVITIEESRG 180
 QY 181 METELEVEGMOFDRGYLSQYVWTDNEKVADELNPFLITDKKVSNIQDILPLEEVLK 240
 DB 181 MOTELDVVEGMOFDRGYLSQYVWTDNEKVADELNPFLITDKKVSNIQDILPLEEVLK 240
 QY 241 TNRPPLIADVDGEALPTLVLRKIRGTFENVAAKAPGDRKKAQLEHLALITGCTVIT 300
 DB 241 TNRPPLIADVDGEALPTLVLRKIRGTFENVAAKAPGDRKKAQLEHLALITGCTVIT 300
 QY 301 EDLGELEKDATMTALGOAAKITVDKSTVIEGSSSEPAIARALIKSLETTSDPR 360
 DB 301 EELGDLKDATMTALGOAAKITVDKSTVIEGSSSEPAIARALIKSLETTSDPR 360
 QY 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNTRAAVEGIVAGGATLTV 420
 DB 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNTRAAVEGIVAGGATLTV 420
 QY 421 IEKVAALESGDAGTGRNIVLRALPEVROIALNAGVSGSVVIDKLNSPAGTGFNAATG 480
 DB 421 IALDLKSESDIQTGINIVLRALPEVROIALNAGVSGSVVIDKLNSPAGTGFNAATG 480
 QY 481 EYVDMIKTGIIDPVKVTASALONAAVSLITTEAVVANKPEPATPAPAMPAGMDPGM 540
 DB 481 QVNMIEEGIVDPKVTASALONAAVSLITTEAVVANKPEPATPAPAMP-MDPSM- 536
 QY 541 GGMGG 545
 DB 537 -GMMG 540

RESULT 5

S32106

groEL protein - Lactococcus lactis

C:Species: Lactococcus lactis

C:Date: 06-Jan-1993 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999

C:Accession: S32106

R:Batt, C.A.

Submitted to the EMBL Data Library, March 1993

A:Reference number: S32105

A:Accession: S32106

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-542 <BAT>

A:Cross-references: EMBL:X71132; NID:g287869; PID:CAA50446.1; PID:g287871

C:Superfamily: chaperonin groEL

Query Match

Best Local Similarity 80.4%; Pred. No. 5.3e-101;

Matches 438; Conservative 53; Mismatches 49; Indels 5; Gaps 3;

QY 1 MAKEKFSADARAAMRGVDMADPTVKTGLPGKRNVLKAFSGPLITNDGVTAKKE 60
 DB 1 MSKDIKFSDDARTAMRGIDILADVTITGLPGKRNVLKAFSGPLITNDGVTAKKE 60
 QY 61 LEHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120
 DB 61 LEHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120
 QY 121 TATATAVEALKAIAPVSGKEALIAOVAVSSRSSEKVEYISEAMERVNDGVITIEESRG 180
 DB 121 LAETVAVASIKEMAIPIVHDKSAIAQAVTSSRSSEKVEYISDAMERVNDGVITIEESRG 180
 QY 181 METELEVEGMOFDRGYLSQYVWTDNEKVADELNPFLITDKKVSNIQDILPLEEVLK 240
 DB 181 MOTELDVVEGMOFDRGYLSQYVWTDNEKVADELNPFLITDKKVSNIQDILPLEEVLK 240
 QY 241 TNRPPLIADVDGEALPTLVLRKIRGTFENVAAKAPGDRKKAQLEHLALITGCTVIT 300
 DB 241 TNRPPLIADVDGEALPTLVLRKIRGTFENVAAKAPGDRKKAQLEHLALITGCTVIT 300
 QY 301 EDLGELEKDATMTALGOAAKITVDKSTVIEGSSSEPAIARALIKSLETTSDPR 360
 DB 301 EELGDLKDATMTALGOAAKITVDKSTVIEGSSSEPAIARALIKSLETTSDPR 360
 QY 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNTRAAVEGIVAGGATLTV 420
 DB 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNTRAAVEGIVAGGATLTV 420
 QY 421 IEKVAALESGDAGTGRNIVLRALPEVROIALNAGVSGSVVIDKLNSPAGTGFNAATG 480
 DB 421 IALDLKSESDIQTGINIVLRALPEVROIALNAGVSGSVVIDKLNSPAGTGFNAATG 480
 QY 481 EYVDMIKTGIIDPVKVTASALONAAVSLITTEAVVANKPEPATPAPAMPAGMDPGM 540
 DB 481 QVNMIEEGIVDPKVTASALONAAVSLITTEAVVANKPEPATPAPAMP-MDPSM- 536
 QY 541 GGMGG 545
 DB 537 -GMMG 540

RESULT 6

AD1333

Class I heat-shock protein (chaperonin) GroEL (imported) - Listeria monocytogenes

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AD1333

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; B.

D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; F.

S.; Jones, L.M.; Karsic, U.

Science 294, 849-852, 2001

A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurpakt, G.; Madueno, E.; Maltournam,

ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; We

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; M0ID:21537279; PMID:11679669

A:Accession: AD1333

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-542 <GLA>

A:Cross-references: GB:NC_003210; PID:NC_003210; PID:g16411538; GSRDB:GN00177

A:Experimental source: strain EGo-e

C:Genetics:
A:Gene: groEL
C:Superfamily: Chaperonin groEL

Query Match 76.4%: Score 2033.5; DB 2; Length 542;
Best Local Similarity 75.6%: Pred. No. 3.9e-94;
Matches 412; Conservative 61; Mismatches 67; Indels 5; Gaps 3;

```

Oy 1 MAKEIKTSADARAAWYRGVMDLADTVKTLGPKGRNVYLEKAFSPILITNDGVTIAKEIE 60
    |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 1 MAKDIKTSADARAAWYRGVMDLANAVKYLGRKGRNVYLEKAFSPILITNDGVTIAKEIE 60
Oy 61 LEDPENNKGALVSEVASTNDVAGDGTATATVLAQMIQEGKLNVTAGANPVGVRGIE 120
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 61 LEDPENNKGALVSEVASTNDVAGDGTATATVLAQMIQEGKLNVTAGANPVGVRGIE 120
Oy 121 TATATVETALKAIAQVPSGKEAIAQVAAVSSSEKVEGYISEAMERNVNDGVITIEESRG 180
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 121 KAAVATAEELKAISKPIESKESIAQVAAVSSSEKVEGYISEAMERNVNDGVITIEESRG 180
Oy 181 METELEVEGKQDFRGYLSQVYVTDNEKNVADLENPFILITDKKVSNTODILPLEEVLK 240
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 181 FATELDVVEGKQDFRGYLSQVYVTDNEKNVADLENPFILITDKKVSNTODILPLEEVLK 240
Oy 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVAKPGFGRKKAMLEDAIILTGCVIT 300
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 241 OGRPLLIADVEGEAQAATLVNKRIGTFNNVAVAKPGFGRKKAMLEDAIILTGCVIT 300
Oy 301 EDLGELEKDATMTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSQLETTSPDR 360
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 301 EDLGELEKDATMTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSQLETTSPDR 360
Oy 361 EKLOERLAKLAGVAIVKYGAPETALKEKRLIEDALNATRAVEGIVAGGATLTV 420
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 361 EKLOERLAKLAGVAIVKYGAPETALKEKRLIEDALNATRAVEGIVAGGATLTV 420
Oy 421 IEKVALELEDGDATGRNIVLALPEPVROIALNAGIEGVSVIDIKKSPAGTGFNAATG 480
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 421 YKKVALELEDGDATGRNIVLALPEPVROIALNAGIEGVSVIDIKKSPAGTGFNAATG 480
Oy 481 EYWDNKTGIIIDPVKVTSSALONAAVASLILTEAVVANKPEPATPAPAMPAGDQGM 540
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 481 EYWNNDMGIVDPKVTSSALONAAVASLILTEAVVADKPDENGA-APV---DMG-M 535
Oy 541 GGMG 545
    |||:|||||
Db 536 GGMG 540

```

RESULT 7

AC1104
C:Species: *Listeria innocua* (chaperonin) groEL (imported) - *Listeria innocua* (strain Clif
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AC1104
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
R:Glaser, P.; Frangoul, L.; Buchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournan, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1104
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-542 <GLA>
A:Cross-references: GB:AL592023; PIDN:CMC97403.1; PID:g16414687, GSPDB:GN00178
A:Experimental source: strain Clif11262
C:Genetics: groEL
A:Gene: groEL
C:Superfamily: chaperonin groEL

Query Match 76.1%: Score 2026.5; DB 2; Length 542;
Best Local Similarity 75.0%: Pred. No. 8.8e-94;
Matches 409; Conservative 62; Mismatches 69; Indels 5; Gaps 2;

```

Oy 1 MAKEIKTSADARAAWYRGVMDLADTVKTLGPKGRNVYLEKAFSPILITNDGVTIAKEIE 60
    |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 1 MAKDIKTSADARAAWYRGVMDLANAVKYLGRKGRNVYLEKAFSPILITNDGVTIAKEIE 60
Oy 61 LEDPENNKGALVSEVASTNDVAGDGTATATVLAQMIQEGKLNVTAGANPVGVRGIE 120
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 61 LEDPENNKGALVSEVASTNDVAGDGTATATVLAQMIQEGKLNVTAGANPVGVRGIE 120
Oy 121 TATATVETALKAIAQVPSGKEAIAQVAAVSSSEKVEGYISEAMERNVNDGVITIEESRG 180
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 121 KAAVATAEELKAISKPIESKESIAQVAAVSSSEKVEGYISEAMERNVNDGVITIEESRG 180
Oy 181 METELEVEGKQDFRGYLSQVYVTDNEKNVADLENPFILITDKKVSNTODILPLEEVLK 240
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 181 FATELDVVEGKQDFRGYLSQVYVTDNEKNVADLENPFILITDKKVSNTODILPLEEVLK 240
Oy 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVAKPGFGRKKAMLEDAIILTGCVIT 300
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 241 OGRPLLIADVEGEAQAATLVNKRIGTFNNVAVAKPGFGRKKAMLEDAIILTGCVIT 300
Oy 301 EDLGELEKDATMTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSQLETTSPDR 360
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 301 EDLGELEKDATMTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSQLETTSPDR 360
Oy 361 EKLOERLAKLAGVAIVKYGAPETALKEKRLIEDALNATRAVEGIVAGGATLTV 420
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 361 EKLOERLAKLAGVAIVKYGAPETALKEKRLIEDALNATRAVEGIVAGGATLTV 420
Oy 421 IEKVALELEDGDATGRNIVLALPEPVROIALNAGIEGVSVIDIKKSPAGTGFNAATG 480
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 421 YKKVALELEDGDATGRNIVLALPEPVROIALNAGIEGVSVIDIKKSPAGTGFNAATG 480
Oy 481 EYWDNKTGIIIDPVKVTSSALONAAVASLILTEAVVANKPEPATPAPAMPAGDQGM 540
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 481 EYWNNDMGIVDPKVTSSALONAAVASLILTEAVVADKPDENGA---AGDMG-M 535
Oy 541 GGMG 545
    |||:|||||
Db 536 GGMG 540

```

RESULT 8

B41884
58k heat shock protein groEL - *Bacillus subtilis*
N:Alternate names: class I heat-shock protein (chaperonin) groEL
C:Species: *Bacillus subtilis*
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: B41884; B41885; J01372; B47683; D69637
R:Li, M.; Wong, S.L.
J. Bacteriol. 174, 3981-3992, 1992
A:Title: Cloning and characterization of the groESL operon from *Bacillus subtilis*.
A:Reference number: A41884; MUID:92283753; PMID:1350776
A:Accession: B41884
A:Molecule type: DNA
A:Residues: 1-544
A:Cross-references: GB:M81132; NID:g143025; PIDN:AAA2503.1; PID:g143027
A:Experimental source: strain 168
A>Note: Sequence extracted from NCBI backbone (NCBIN:105982, NCBI:P.105989)
R:Schmidt, A.; Schlesswohl, M.; Volker, U.; Hecker, M.; Schumann, W.
J. Bacteriol. 174, 3993-3999, 1992
A:Title: Cloning, sequencing, mapping, and transcriptional analysis of the groESL op
A:Reference number: A41885; MUID:92283754; PMID:1350777
A:Accession: B41885
A:Molecule type: DNA
A:Residues: 1-544 <SCH>
A:Cross-references: GB:M84965; NID:g143061; PIDN:AAA22531.1; PID:g143063
A:Experimental source: strain MB1
A>Note: Sequence extracted from NCBI backbone (NCBIN:105432, NCBI:P.105434)
R:Itazawa, Y.; Yoshikawa, H.; Kawamura, F.; Itaya, M.; Takahashi, H.

Biosci. Biotechnol. Biochem. 56, 1995-2002, 1992
 A:Title: Isolation and characterization of the groES and groEL genes of *Bacillus subtilis*
 A:Reference number: JCI371; MUID:93129852; PMID:1369494
 A:Accession: JCI372
 A:Molecule type: DNA
 A:Residues: 1-14, 'N', 16-124, 'L', 126-201, 'L', 203-374, 'R', 376-544 <TO2>
 A:Cross-references: GB:DI0972; GB:DI01157; NID:94433779; PIDN:BA22519.1; PID:94433781
 A:Experimental source: strain Marburg 168
 A:Note: the authors translated the codon AAT for residue 15 as Met
 J. Volker, U. Mach, H. Schmid, R. Hecker, M.
 J. Gen. Microbiol. 138, 2123-2135, 1992
 A:Title: Stress proteins and cross-protection by heat shock and salt stress in *Bacillus*
 A:Reference number: A47683; MUID:93123969; PMID:1362210
 A:Contents: IS58
 A:Accession: B47683
 A:Molecule type: protein
 A:Residues: 2-31 <VOL>
 A:Note: sequence extracted from NCBI backbone (NCBI:121871)
 R. Kunst, F. Ogasawara, N. Moszer, I. Albertini, A.M. Alloni, G. Azavedo, V. Bertet, C. Bron, S. Brouillet, S. Brusch, C.V. Caldwell, B. Capuano, V. Carter, N.M. Cho, Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizel, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hiltbert, R.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koeltter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogawa, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet, A.; Rieger, M.; Rivolta, C.; Kocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Schuster, S.; Schuster, R.; Scott, R.; Scott, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Whalers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: D69637
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-544 <UN>
 A:Cross-references: GB:299107; GB:AL009126; NID:92632866; PIDN:CA12422.1; PID:92632916
 A:Experimental source: strain 168
 C:Genetic: groEL
 C:Gene: groEL
 C:Superfamily: chaperonin groEL
 C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 76.18; Score 2026.5; DB 2; Length 544;
 Best Local Similarity 73.88; Pred. No. 8.8e-94;
 Matches 402; Conservative 69; Mismatches 71; Indels 3; Gaps 1;

QY 1 MAKEIKFSADARAANVGVMDLADYKVTGPGKGRNVLEKAGSPPLITNDGVTIAKEIE 60
 DB 1 MAKEIKFSADARAANVGVMDLADYKVTGPGKGRNVLEKAGSPPLITNDGVTIAKEIE 60
 QY 61 LEDHEFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120
 DB 61 LEDHEFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120
 QY 121 TATATAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRGNGCVITIEESRG 180
 DB 121 TATATAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRGNGCVITIEESRG 180
 QY 181 MEPELEVEGMOGDRGYLSQYMTDNEMKVAADLENPILITDKKSNIDILPLEEYVK 240
 DB 181 MEPELEVEGMOGDRGYLSQYMTDNEMKVAADLENPILITDKKSNIDILPLEEYVK 240
 QY 241 TNRPLITADVDGEALPTLVNKRIGTFNVAAKAPGFGDRRKAMEDIAITLGSTVIT 300
 DB 241 TNRPLITADVDGEALPTLVNKRIGTFNVAAKAPGFGDRRKAMEDIAITLGSTVIT 300
 QY 301 EDLGLKDATMTALGOAANKITVDKSTVIEGSGSSEAIAANRITALIKSOLETTSDPR 360
 DB 301 EDLGLKDATMTALGOAANKITVDKSTVIEGSGSSEAIAANRITALIKSOLETTSDPR 360
 QY 481 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 480
 DB 481 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 480
 QY 481 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 480
 DB 481 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 480
 QY 541 GGMGG 545
 DB 541 GGMGG 545

RESULT 9
 B49855
 A:Title: Isolation and characterization of the groES and groEL genes of *Bacillus subtilis*
 A:Reference number: JCI371; MUID:93129852; PMID:1369494
 A:Accession: JCI372
 A:Molecule type: DNA
 A:Residues: 1-14, 'N', 16-124, 'L', 126-201, 'L', 203-374, 'R', 376-544 <TO2>
 A:Cross-references: GB:DI0972; GB:DI01157; NID:94433779; PIDN:BA22519.1; PID:94433781
 A:Experimental source: strain Marburg 168
 A:Note: the authors translated the codon AAT for residue 15 as Met
 J. Volker, U. Mach, H. Schmid, R. Hecker, M.
 J. Gen. Microbiol. 138, 2123-2135, 1992
 A:Title: Stress proteins and cross-protection by heat shock and salt stress in *Bacillus*
 A:Reference number: A47683; MUID:93123969; PMID:1362210
 A:Contents: IS58
 A:Accession: B47683
 A:Molecule type: protein
 A:Residues: 2-31 <VOL>
 A:Note: sequence extracted from NCBI backbone (NCBI:121871)
 R. Kunst, F. Ogasawara, N. Moszer, I. Albertini, A.M. Alloni, G. Azavedo, V. Bertet, C. Bron, S. Brouillet, S. Brusch, C.V. Caldwell, B. Capuano, V. Carter, N.M. Cho, Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizel, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hiltbert, R.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koeltter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogawa, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet, A.; Rieger, M.; Rivolta, C.; Kocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Schuster, S.; Schuster, R.; Scott, R.; Scott, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Whalers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: D69637
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-544 <UN>
 A:Cross-references: GB:299107; GB:AL009126; NID:92632866; PIDN:CA12422.1; PID:92632916
 A:Experimental source: strain 168
 C:Genetic: groEL
 C:Gene: groEL
 C:Superfamily: chaperonin groEL
 C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 75.98; Score 2021.5; DB 2; Length 539;
 Best Local Similarity 74.98; Pred. No. 1.5e-93;
 Matches 408; Conservative 63; Mismatches 65; Indels 9; Gaps 2;

QY 1 MAKEIKFSADARAANVGVMDLADYKVTGPGKGRNVLEKAGSPPLITNDGVTIAKEIE 60
 DB 1 MAKEIKFSADARAANVGVMDLADYKVTGPGKGRNVLEKAGSPPLITNDGVTIAKEIE 60
 QY 61 LEDHEFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120
 DB 61 LEDHEFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120
 QY 121 TATATAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRGNGCVITIEESRG 180
 DB 121 TATATAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRGNGCVITIEESRG 180
 QY 181 MEPELEVEGMOGDRGYLSQYMTDNEMKVAADLENPILITDKKSNIDILPLEEYVK 240
 DB 181 MEPELEVEGMOGDRGYLSQYMTDNEMKVAADLENPILITDKKSNIDILPLEEYVK 240
 QY 241 TNRPLITADVDGEALPTLVNKRIGTFNVAAKAPGFGDRRKAMEDIAITLGSTVIT 300
 DB 241 TNRPLITADVDGEALPTLVNKRIGTFNVAAKAPGFGDRRKAMEDIAITLGSTVIT 300
 QY 301 EDLGLKDATMTALGOAANKITVDKSTVIEGSGSSEAIAANRITALIKSOLETTSDPR 360
 DB 301 EDLGLKDATMTALGOAANKITVDKSTVIEGSGSSEAIAANRITALIKSOLETTSDPR 360
 QY 361 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 420
 DB 361 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 420
 QY 421 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 480
 DB 421 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 480
 QY 481 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 539
 DB 481 EKVYALAELEGGDAGTGRNIVLRALEPEPYROTALNAGCEGVYIDKLNKPAGTGNATG 539

A:Reference number: J01194; MUID:91354309; PMID:1679330
 A:Accession: J01195
 A:Molecule type: DNA
 A:Residues: 1-538 <RAW>
 A:Note: part of this sequence, including both the amino and carboxyl ends of the mature
 A:Note: the nucleotide sequence residues 531-538 is not shown in this paper
 A:Other: T.; Honda, K.; Saito, K.; Hayashi, H.; Iano, H.; Hamamoto, T.; Kagawa, Y.
 A:Title: Heat shock promoter of the *mopH* operon.
 A:Reference number: J01479; MUID:93213292; PMID:8096382
 A:Accession: F01252
 A:Molecule type: DNA
 A:Residues: 1-79 <OHF>
 C:Comment: This protein is essential for the formation and restoration of many supramole
 C:Superfamily: chaperonin groEL
 C:Keywords: heat shock; stress-induced protein

Query Match 74.4%; Score 1981; DB 2; Length 538;
 Best Local Similarity 73.7%; Pred. No. 1, 6e-91;
 Matches 400; Conservative 64; Mismatches 73; Indels 6; Gaps 1;

QY 1 MAKEIFSDAARAVRGVMDLADYVYTGPRGRNVYLEKAFSGPLTNDGYTAKKEIE 60
 DB 1 MAKQKFSRARRMLRGVMDLADYVYTGPRGRNVYLEKAFSGPLTNDGYTAKKEIE 60
 QY 61 LEDHFENMGAKLYEVAASKTNDIAGDGTATVLAQAIHVEGLKNTAGANPIGIRGIE 120
 DB 61 LEDHFENMGAKLYEVAASKTNDIAGDGTATVLAQAIHVEGLKNTAGANPIGIRGIE 120
 QY 121 TATATAVEALKAIAQVSGKEAIAQVAASVSSSEKGEYISEAMERVNDGVITIEESRG 180
 DB 121 TATATAVEALKAIAQVSGKEAIAQVAASVSSSEKGEYISEAMERVNDGVITIEESRG 180
 QY 181 METELEVEGMOFDRGYLSOYWTNDENKVAADLENPFLITTKKVSNIODILPLEEVLK 240
 DB 181 FTELEVEGMOFDRGYLSOYWTNDENKVAADLENPFLITTKKVSNIODILPLEEVLK 240
 QY 241 TNRPLIITADVDGALPTLVNKRIGTFENVVAAPGFGDRKKALEDIAITLGTVIT 300
 DB 241 OGRPLIITADVDGALPTLVNKRIGTFENVVAAPGFGDRKKALEDIAITLGTVIT 300
 QY 301 EDGLGELKDATMTALGOAAKITVDKSTVYVSGSSSEAIANRIALIKSOLETTSDPFR 360
 DB 301 EDGLGELKSTTASIGRAKSVYVTKETITVEGAGOSKRIKAIINQIAQLETTSEDFR 360
 QY 361 EKIOLERLAKLAGVAIVKCAPETELKEMKRLIEDALNTRAAYEGIVAGGCTALTIV 420
 DB 361 EKIOLERLAKLAGVAIVKCAPETELKEMKRLIEDALNTRAAYEGIVAGGCTALTIV 420
 QY 421 IEKVAALEGGDGTATGRNIVLRALEPEYROTALNAGYEGSVYIDKLNSPAGTGNATG 480
 DB 421 HNKVAAIEEGDEATGVKIVLRAIEEPYROTALNAGLEGGIVYERLKNKPGIGNATG 480
 QY 481 EYVDMIKTGIIDPVKTRSAIONAASVSLITTEVAVNKPPEATPAPAMPAGMDPGM 540
 DB 481 EYVDMIEAGIYDPTKTRSAIONAASVSLITTEVAVNKPPEATPAPAMPAGMDPGM 540
 QY 541 GGM 543
 DB 535 GGM 537

RESULT 13
 J05130 heat shock protein groEL - Bacillus sp.
 C:Species: Bacillus sp.
 C:Date: 05-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: J05130
 R:Kurda, M.; Ohta, T.; Kudo, T.; Kobayashi, T.; Saito, K.; Hayashi, H.; Hamamoto, T.; Kagawa, Y.
 A:Title: Molecular cloning and nucleotide sequence of the groEL gene from the alkaliphilic
 A:Reference number: J05130; MUID:97141316; PMID:8987660
 A:Accession: J05130

A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-544 <XUA>
 A:Cross-references: DDBJ:D55630; NID:91682949; PIDN:BA09494.1; PID:91682951
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: groEL
 C:Superfamily: chaperonin groEL

Query Match 73.6%; Score 1959.5; DB 2; Length 544;
 Best Local Similarity 72.6%; Pred. No. 1, 9e-90;
 Matches 397; Conservative 73; Mismatches 70; Indels 7; Gaps 5;

QY 1 MAKEIFSDAARAVRGVMDLADYVYTGPRGRNVYLEKAFSGPLTNDGYTAKKEIE 60
 DB 1 MAKQKFSRARRMLRGVMDLADYVYTGPRGRNVYLEKAFSGPLTNDGYTAKKEIE 60
 QY 61 LEDHFENMGAKLYEVAASKTNDIAGDGTATVLAQAIHVEGLKNTAGANPIGIRGIE 120
 DB 61 LEDHFENMGAKLYEVAASKTNDIAGDGTATVLAQAIHVEGLKNTAGANPIGIRGIE 120
 QY 121 TATATAVEALKAIAQVSGKEAIAQVAASVSSSEKGEYISEAMERVNDGVITIEESRG 180
 DB 121 TATATAVEALKAIAQVSGKEAIAQVAASVSSSEKGEYISEAMERVNDGVITIEESRG 180
 QY 181 METELEVEGMOFDRGYLSOYWTNDENKVAADLENPFLITTKKVSNIODILPLEEVLK 240
 DB 181 FTELEVEGMOFDRGYLSOYWTNDENKVAADLENPFLITTKKVSNIODILPLEEVLK 240
 QY 241 TNRPLIITADVDGALPTLVNKRIGTFENVVAAPGFGDRKKALEDIAITLGTVIT 300
 DB 241 OGRPLIITADVDGALPTLVNKRIGTFENVVAAPGFGDRKKALEDIAITLGTVIT 300
 QY 301 EDGLGELKDATMTALGOAAKITVDKSTVYVSGSSSEAIANRIALIKSOLETTSDPFR 360
 DB 301 EDGLGELKSTTASIGRAKSVYVTKETITVEGAGOSKRIKAIINQIAQLETTSEDFR 360
 QY 361 EKIOLERLAKLAGVAIVKCAPETELKEMKRLIEDALNTRAAYEGIVAGGCTALTIV 420
 DB 361 EKIOLERLAKLAGVAIVKCAPETELKEMKRLIEDALNTRAAYEGIVAGGCTALTIV 420
 QY 420 VIEKVAALEGGDGTATGRNIVLRALEPEYROTALNAGYEGSVYIDKLNSPAGTGNATG 479
 DB 420 VIEKVAALEGGDGTATGRNIVLRALEPEYROTALNAGYEGSVYIDKLNSPAGTGNATG 479
 QY 480 EYVDMIKTGIIDPVKTRSAIONAASVSLITTEVAVNKPPEATPAPAMPAGMDPGM 538
 DB 480 EYVDMIEAGIYDPTKTRSAIONAASVSLITTEVAVNKPPEATPAPAMPAGMDPGM 538
 QY 539 GGM 545
 DB 536 GGM 542

RESULT 14
 C89994 groEL protein [Imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89994
 R:Kurda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Cui, L.;
 ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Saito, C.; Sekimizu,
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:1141816
 A:Accession: C89994
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-538 <XUA>
 A:Cross-references: GB:BA000018; PID:913701023; PIDN:BA03116.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:

A:Gene: groEL
C:Superfamily: chaperonin groEL

Query Match 71.5%; Score 1905; Db 2; Length 538;
Best Local Similarity 69.8%; Pred. No. 9,7e-88;

Matches 377; Conservative 78; Mismatches 83; Indels 2; Gaps 2;

```
OY 1 MAKIKFSADAAAVGVMDLADVTYKVTLPKRRNVLEKFGSPILITIDGVTIAKIE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MVKOLKESDARQAMLRGVQDLANAVKVTIGPKRRNVLDKKEFTAPLITIDGVTIAKIE 60
OY 61 LEDHFENMGAKLYEVASKTNDIAGDGTATVLTQAIYHEGLKNVTAGANPIRGRIE 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LEDPYENMGAKLYEVASKTNDIAGDGTATVLTQAIYHEGLKNVTAGANPIRGRIE 120
OY 61 LEDPYENMGAKLYEVASKTNDIAGDGTATVLTQAIYHEGLKNVTAGANPIRGRIE 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LEDPYENMGAKLYEVASKTNDIAGDGTATVLTQAIYHEGLKNVTAGANPIRGRIE 120
OY 121 TATATVAVLAKIAQPVSGKEALIAOVAVSSRSKGVGYSIEMERNGDCVITIEESRG 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TATATVAVLAKIAQPVSGKEALIAOVAVSSRSKGVGYSIEMERNGDCVITIEESRG 180
OY 121 KAVVAVALHENSOKVENKNEIAQVAISDADEIGRTISAEKVGNDGVITIEESRG 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KAVVAVALHENSOKVENKNEIAQVAISDADEIGRTISAEKVGNDGVITIEESRG 180
OY 161 METFEVVGKQDFRGYLSQYNTDNEKRVADLENPIITDKKVSNIODILPLEEYVK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 161 LNTLEVEGKQDFRGYLSQYNTDNEKRVADLENPIITDKKVSNIODILPLEEYVK 240
OY 241 TNRPLLIADVDGDEALPTLVNKRIGTFENVVAVKAPGFGRRKAMLEDIAIILTGQVIT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 SNRPILIVADEVDGDEALPTLVNKRIGTFENVVAVKAPGFGRRKAMLEDIAIILTGQVIT 300
OY 301 EDLGLLELKDATMTALGQAATVVDKSTVIEGSGSSSEAIANRIALIKSQLETTSDPDR 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 DDLGLLKLKASIDMLGTASKVEYTKDNTVYDGDGSDNSIDARVSQLSQIEETSDPDR 360
OY 361 EKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNAAGVSGVYIDKNSPAGTGPNATG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 EKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNAAGVSGVYIDKNSPAGTGPNATG 420
OY 421 IERVVALELEDGDATGRNIVLRALPEPVROIALNAGVSGVYIDKNSPAGTGPNATG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 YQKVSIELEEDDIETGVNIYKALTAAPVQIAENAGLEGSVYIEERLNAEPVGNATIN 480
OY 481 EMDYDKTKTIIDPVKVTIRSAALONAAVASLITTEAVVANKPEPATPAPMPAGMDPQM 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 EMDYDKTKTIIDPVKVTIRSAALONAAVASLITTEAVVANKPEPATPAPMPAGMDPQM 540
OY 537 GNM 539
```

RESULT 15

JN0601
heat shock protein 60 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
C:Accession: JN0601; P05008
R:Ohta, T.; Honda, K.; Kuroda, M.; Saito, K.; Hayashi, H.
Biochem. Biophys. Res. Commun. 193, 730-737, 1993
A:Title: Molecular characterization of the gene operon of heat shock proteins hsp60 and
A:Reference number: JN0600; M01D:93290669; PMID:7916607
A:Accession: JN0601
A:Molecule type: DNA
A:Residues: 1-539 <OH1>
A:Accession: P05008
A:Molecule type: Protein
A:Residues: 1-21 <OH2>
C:Genetics:
A:Gene: hsp60
C:Superfamily: chaperonin groEL
C:Keywords: heat shock; stress-induced protein

Query Match 69.4%; Score 1847.5; Db 2; Length 539;
Best Local Similarity 68.3%; Pred. No. 7.1e-85;
Matches 371; Conservative 78; Mismatches 87; Indels 7; Gaps 4;

```
OY 1 MAKEIFSDARAAVGVMDLADVTYKVTLPKRRNVLEKFGSPILITIDGVTIAKIE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MVKOLKESDARQAMLRGVQDLANAVKVTIGPKRRNVLDKKEFTAPLITIDGVTIAKIE 60
```

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OY 61 LEDHFENMGAKLYEVASKTNDIAGDGTATVLTQAIYHEGLKNVTAGANPIRGRIE 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LEDPYENMGAKLYEVASKTNDIAGDGTATVLTQAIYHEGLKNVTAGANPIRGRIE 120
OY 121 TATATVAVLAKIAQPVSGKEALIAOVAVSSRSKGVGYSIEMERNGDCVITIEESRG 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TATATVAVLAKIAQPVSGKEALIAOVAVSSRSKGVGYSIEMERNGDCVITIEESRG 180
OY 121 KAVVAVALHENSOKVENKNEIAQVAISDADEIGRTISAEKVGNDGVITIEESRG 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KAVVAVALHENSOKVENKNEIAQVAISDADEIGRTISAEKVGNDGVITIEESRG 180
OY 178 SGMGTELEVBEKQDFRGYLSQYNTDNEKRVADLENPIITDKKVSNIODILPLEEYVK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SGRLEVELEL--QMGDFRGYLSQYNTDNEKRVADLENPIITDKKVSNIODILPLEEYVK 240
OY 238 VLKTRPLLIADVDGDEALPTLVNKRIGTFENVVAVKAPGFGRRKAMLEDIAIILTGQVIT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 VVQSNRPILIVADEVDGDEALPTLVNKRIGTFENVVAVKAPGFGRRKAMLEDIAIILTGQVIT 300
OY 298 VITEDGLLELKDATMTALGQAATVVDKSTVIEGSGSSSEAIANRIALIKSQLETTSDPDR 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 VITEDGLLELKDATMTALGQAATVVDKSTVIEGSGSSSEAIANRIALIKSQLETTSDPDR 360
OY 358 FDRKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNTRAIVEGIVAGGTAL 417
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 FDRKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNTRAIVEGIVAGGTAL 417
OY 418 ITVIEKVALELEDGDATGRNIVLRALPEPVROIALNAGVSGVYIDKNSPAGTGPNATG 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 VAVVQKVSSEAEAGDIETGVNIYKALTAAPVQIAENAGLEGSVYIEERLNAEPVGNATIN 477
OY 478 ATGEVDMITGTIDPVKVTIRSAALONAAVASLITTEAVVANKPEPATPAPMPAGMDPQM 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 ATGEVDMITGTIDPVKVTIRSAALONAAVASLITTEAVVANKPEPATPAPMPAGMDPQM 540
OY 537 GNM 540
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Search completed: April 8, 2003, 14:25:19
Job time : 23 secs